

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/527,708
Source: PCT
Date Processed by STIC: 3-25-05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 03/25/2005

PATENT APPLICATION: US/10/527,708

TIME: 08:52:43

Input Set : A:\3097US0P seq.txt

Output Set: N:\CRF4\03252005\J527708.raw

3 <110> APPLICANT: MATSUI, Hideki
 4 WATANABE, Tomomichi
 6 <120> TITLE OF INVENTION: Preventives/remedies for neurodegenerative disease
 8 <130> FILE REFERENCE: 3097 US0P
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/527,708
 C--> 10 <141> CURRENT FILING DATE: 2005-03-11
 10 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/011631
 11 <151> PRIOR FILING DATE: 2003-09-11
 13 <150> PRIOR APPLICATION NUMBER: JP2002-269091
 14 <151> PRIOR FILING DATE: 2002-09-13
 16 <160> NUMBER OF SEQ ID NOS: 25
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 358
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Homo sapience
 23 <400> SEQUENCE: 1
 24 Met Arg Ala Thr Pro Leu Ala Ala Pro Ala Gly Ser Leu Ser Arg Lys
 25 5 10 15
 26 Lys Arg Leu Glu Leu Asp Asp Asn Leu Asp Thr Glu Arg Pro Val Gln
 27 20 25 30
 28 Lys Arg Ala Arg Ser Gly Pro Gln Pro Arg Leu Pro Pro Cys Leu Leu
 29 35 40 45
 30 Pro Leu Ser Pro Pro Thr Ala Pro Asp Arg Ala Thr Ala Val Ala Thr
 31 50 55 60
 32 Ala Ser Arg Leu Gly Pro Tyr Val Leu Leu Glu Pro Glu Glu Gly Gly
 33 65 70 75 80
 34 Arg Ala Tyr Gln Ala Leu His Cys Pro Thr Gly Thr Glu Tyr Thr Cys
 35 85 90 95
 36 Lys Val Tyr Pro Val Gln Glu Ala Leu Ala Val Leu Glu Pro Tyr Ala
 37 100 105 110
 38 Arg Leu Pro Pro His Lys His Val Ala Arg Pro Thr Glu Val Leu Ala
 39 115 120 125
 40 Gly Thr Gln Leu Leu Tyr Ala Phe Phe Thr Arg Thr His Gly Asp Met
 41 130 135 140
 42 His Ser Leu Val Arg Ser Arg His Arg Ile Pro Glu Pro Glu Ala Ala
 43 145 150 155 160
 44 Val Leu Phe Arg Gln Met Ala Thr Ala Leu Ala His Cys His Gln His
 45 165 170 175
 46 Gly Leu Val Leu Arg Asp Leu Lys Leu Cys Arg Phe Val Phe Ala Asp
 47 180 185 190
 48 Arg Glu Arg Lys Lys Leu Val Leu Glu Asn Leu Glu Asp Ser Cys Val
 49 195 200 205
 50 Leu Thr Gly Pro Asp Asp Ser Leu Trp Asp Lys His Ala Cys Pro Ala

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51      210      215      220
52 Tyr Val Gly Pro Glu Ile Leu Ser Ser Arg Ala Ser Tyr Ser Gly Lys
53 225      230      235      240
54 Ala Ala Asp Val Trp Ser Leu Gly Val Ala Leu Phe Thr Met Leu Ala
55      245      250      255
56 Gly His Tyr Pro Phe Gln Asp Ser Glu Pro Val Leu Leu Phe Gly Lys
57      260      265      270
58 Ile Arg Arg Gly Ala Tyr Ala Leu Pro Ala Gly Leu Ser Ala Pro Ala
59      275      280      285
60 Arg Cys Leu Val Arg Cys Leu Leu Arg Arg Glu Pro Ala Glu Arg Leu
61      290      295      300
62 Thr Ala Thr Gly Ile Leu Leu His Pro Trp Leu Arg Gln Asp Pro Met
63 305      310      315      320
64 Pro Leu Ala Pro Thr Arg Ser His Leu Trp Glu Ala Ala Gln Val Val
65      325      330      335
66 Pro Asp Gly Leu Gly Leu Asp Glu Ala Arg Glu Glu Glu Gly Asp Arg
67      340      345      350
68 Glu Val Val Leu Tyr Gly
69      355
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72 <211> LENGTH: 1074
73 <212> TYPE: DNA
74 <213> ORGANISM: Homo sapience
76 <400> SEQUENCE: 2
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78 ttggatgaca acttagatac cgagcgtccc gtccagaaac gagctcgaag tgggccccag 120
79 cccagactgc cccctgcct gttgcccctg agcccaccta ctgctccaga tcgtgcaact 180
80 gctgtggcca ctgcctcccg tcttggggcc tatgtcctcc tggagcccga ggagggcggg 240
81 cgggcctacc aggccttgca ctgccctaca ggcactgagt atacctgcaa ggtgtacccc 300
82 gtccaggaag ccctggccgt gctggagccc tatgcgcggc tgcccccgca caagcatgtg 360
83 gctcgggcca ctgaggtcct ggctgggtacc cagctcctct acgccttttt cactcggacc 420
84 catggggaca tgcacagcct ggtgcgaagc cgccaccgta tccctgagcc tgaggctgcc 480
85 gtgctcttcc gccagatggc caccgccctg gcgcactgtc accagcacgg tctggtcctg 540
86 cgtgatctca agctgtgtcg ctttgtcttc gctgaccgtg agaggaagaa gctggtgctg 600
87 gagaacctgg aggactcctg cgtgctgact gggccagatg attcctctgt ggacaagcac 660
88 gcgtgcccag cctacgtggg acctgagata ctacagctcac gggcctcata ctcgggcaag 720
89 gcagccgatg tctggagcct gggcgtggcg ctcttcacca tgctggccgg ccactacccc 780
90 ttccaggact cggagcctgt cctgctcttc ggcaagatcc gccgcggggc ctacgccttg 840
91 cctgcaggcc tctcggcccc tgcccgtgt ctggttcgct gcctccttcg tcgggagcca 900
92 gctgaacggc tcacagccac aggcatactc ctgcaccct ggctgcgaca ggacccgatg 960
93 cccttagccc caaccgatc ccatctctgg gaggtgccc aggtggtccc tgatggactg 1020
94 gggctggacg aagccagga agaggagga gacagagaag tggttctgta tggc 1074
96 <210> SEQ ID NO: 3
97 <211> LENGTH: 32
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: Primer
104 <400> SEQUENCE: 3

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105 gccatgcgag ccacccctct ggctgctcct gc 32
107 <210> SEQ ID NO: 4
108 <211> LENGTH: 28
109 <212> TYPE: DNA
110 <213> ORGANISM: Artificial Sequence
112 <220> FEATURE:
113 <223> OTHER INFORMATION: Primer
115 <400> SEQUENCE: 4
116 cctagccata cagaaccact tctctgtc 28
118 <210> SEQ ID NO: 5
119 <211> LENGTH: 1074
120 <212> TYPE: DNA
121 <213> ORGANISM: Homo sapience
123 <400> SEQUENCE: 5
124 atgcgagcca cccctctagc tgctcctgcg gggtccctgt ccaggaagaa gcggttgag 60
125 ttgatgaca acttagatac cgagcgctccc gtccagaaac gagctcgaag tgggccccag 120
126 cccagactgc cccctgcct gttgcccctg agcccaccta ctgctccaga tcgtgcaact 180
127 gctgtggcca ctgcctcccg tcttgggccc tatgtcctcc tggagcccga ggagggcggg 240
128 cgggcctacc aggcctgca ctgccctaca ggcactgagt atacctgcaa ggtgtacccc 300
129 gtccaggaag ccccgccgt gctggagccc tatgcgcggc tgcccccgca caagcatgtg 360
130 gctcggccca ctgaggctcct ggctggtacc cagctcctct acgccttttt cactcggacc 420
131 catggggaca tgcacagcct ggtgcgaagc cgccaccgta tccctgagcc tgaggctgcc 480
132 gtgctcttcc gccagatggc caccgccttg gcgactgtc accagcacgg tctggtcctg 540
133 cgtgatctca agctgtgtcg ctttgtcttc gctgaccgtg agaggaagaa gctggtgctg 600
134 gagaacctgg aggactcctg cgtgctgact gggccagatg attccctgtg ggacaagcac 660
135 gcgtgcccag cctacgtggg acctgagata ctacgtcac gggcctcata ctcgggcaag 720
136 gcagccgatg tctggagcct gggcggtggc ctcttcacca tgctggccgg cactacccc 780
137 ttccaggact cggagcctgt cctgctcttc ggcaagatcc gccgcggggc ctacgccttg 840
138 cctgcaggcc tctcgccccc tgcccgtgt ctgggtcgct gcctccttcg tcgggagcca 900
139 gctgaacggc tcacagccac aggcattctc ctgacccct ggctgcgaca ggacccgatg 960
140 cccttagccc caaccgatc ccatctctgg gaggtgccc aggtggtccc tgatggtctg 1020
141 gggctggacg aagccaggga agaggaggga gacagagaag tggttctgta tggc 1074
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144 <211> LENGTH: 358
145 <212> TYPE: PRT
146 <213> ORGANISM: Homo sapience
148 <400> SEQUENCE: 6
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150 5 10 15
151 Lys Arg Leu Glu Leu Asp Asp Asn Leu Asp Thr Glu Arg Pro Val Gln
152 20 25 30
153 Lys Arg Ala Arg Ser Gly Pro Gln Pro Arg Leu Pro Pro Cys Leu Leu
154 35 40 45
155 Pro Leu Ser Pro Pro Thr Ala Pro Asp Arg Ala Thr Ala Val Ala Thr
156 50 55 60
157 Ala Ser Arg Leu Gly Pro Tyr Val Leu Leu Glu Pro Glu Glu Gly Gly
158 65 70 75 80
159 Arg Ala Tyr Gln Ala Leu His Cys Pro Thr Gly Thr Glu Tyr Thr Cys
160 85 90 95

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161 Lys Val Tyr Pro Val Gln Glu Ala Pro Ala Val Leu Glu Pro Tyr Ala
162          100          105          110
163 Arg Leu Pro Pro His Lys His Val Ala Arg Pro Thr Glu Val Leu Ala
164          115          120          125
165 Gly Thr Gln Leu Leu Tyr Ala Phe Phe Thr Arg Thr His Gly Asp Met
166          130          135          140
167 His Ser Leu Val Arg Ser Arg His Arg Ile Pro Glu Pro Glu Ala Ala
168 145          150          155          160
169 Val Leu Phe Arg Gln Met Ala Thr Ala Leu Ala His Cys His Gln His
170          165          170          175
171 Gly Leu Val Leu Arg Asp Leu Lys Leu Cys Arg Phe Val Phe Ala Asp
172          180          185          190
173 Arg Glu Arg Lys Lys Leu Val Leu Glu Asn Leu Glu Asp Ser Cys Val
174          195          200          205
175 Leu Thr Gly Pro Asp Asp Ser Leu Trp Asp Lys His Ala Cys Pro Ala
176          210          215          220
177 Tyr Val Gly Pro Glu Ile Leu Ser Ser Arg Ala Ser Tyr Ser Gly Lys
178 225          230          235          240
179 Ala Ala Asp Val Trp Ser Leu Gly Val Ala Leu Phe Thr Met Leu Ala
180          245          250          255
181 Gly His Tyr Pro Phe Gln Asp Ser Glu Pro Val Leu Leu Phe Gly Lys
182          260          265          270
183 Ile Arg Arg Gly Ala Tyr Ala Leu Pro Ala Gly Leu Ser Ala Pro Ala
184          275          280          285
185 Arg Cys Leu Val Arg Cys Leu Leu Arg Arg Glu Pro Ala Glu Arg Leu
186          290          295          300
187 Thr Ala Thr Gly Ile Leu Leu His Pro Trp Leu Arg Gln Asp Pro Met
188 305          310          315          320
189 Pro Leu Ala Pro Thr Arg Ser His Leu Trp Glu Ala Ala Gln Val Val
190          325          330          335
191 Pro Asp Gly Leu Gly Leu Asp Glu Ala Arg Glu Glu Glu Gly Asp Arg
192          340          345          350
193 Glu Val Val Leu Tyr Gly
194          355

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196 <210> SEQ ID NO: 7

197 <211> LENGTH: 1074

198 <212> TYPE: DNA

199 <213> ORGANISM: Homo sapience

201 <400> SEQUENCE: 7

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203 ttggatgaca acttagatac cgagcgtccc gtccagaaac gagctcgaag tgggccccag 120
204 cccagactgc ccccttgcc tttgcccctg agcccaccta ctgctccaga tcgtgcaact 180
205 gctgtggcca ctgcctcccg tcttgggccc tatgtcctcc tggagcccga ggagggcgag 240
206 cgggcctacc gggccctgca ctgcctatac ggcactgagt atacctgcaa ggtgtacccc 300
207 gtccaggaag ccccgccgt gctggagccc tatgcgcggc tgccccgca caagcatgtg 360
208 gctcgggcca ctgaggtcct ggctggtacc cagctcctct acgccttttt cactcggacc 420
209 catggggaca tgcacagcct ggtgcgaagc cgccaccgta tccctgagcc tgaggctgcc 480
210 gtgctcttcc gccagatggc caccgccttg gcgcactgtc accagcacgg tctggtcctg 540
211 cgtgatctca agctgtgtcg ctttgtcttc gctgaccgtg agaggaagaa gctggtgctg 600

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212 gagaacctgg aggactcctg cgtgctgact gggccagatg attccctgtg ggacaagcac 660
213 gcgtgcccag cctacgtggg acctgagata ctcagctcac gggcctcata ctcgggcaag 720
214 gcagccgatg tctggagcct gggcgtggcg ctcttcacca tgctggccgg ccactacccc 780
215 ttccaggact cggagcctgt cctgctcttc ggcaagatcc gccgcggggc ctacgccttg 840
216 cctgcaggcc tctcgcccc tgcccgtgt ctggttcgt gcctccttcg tcgggagcca 900
217 gctgaacggc tcacagccac aggcacctc ctgcacccct ggctgcgaca ggacccgatg 960
218 cccttagccc caaccgatc ccatctctgg gaggtgccc aggtggtccc tgatggtctg 1020
219 gggctggacg aagccaggga agaggaggga gacagagaag tggttctgta tggc 1074
221 <210> SEQ ID NO: 8
222 <211> LENGTH: 358
223 <212> TYPE: PRT
224 <213> ORGANISM: Homo sapience
226 <400> SEQUENCE: 8
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230      20      25      30
231 Lys Arg Ala Arg Ser Gly Pro Gln Pro Arg Leu Pro Pro Cys Leu Leu
232      35      40      45
233 Pro Leu Ser Pro Pro Thr Ala Pro Asp Arg Ala Thr Ala Val Ala Thr
234      50      55      60
235 Ala Ser Arg Leu Gly Pro Tyr Val Leu Leu Glu Pro Glu Glu Gly Gly
236 65      70      75      80
237 Arg Ala Tyr Arg Ala Leu His Cys Pro Thr Gly Thr Glu Tyr Thr Cys
238      85      90      95
239 Lys Val Tyr Pro Val Gln Glu Ala Pro Ala Val Leu Glu Pro Tyr Ala
240      100     105     110
241 Arg Leu Pro Pro His Lys His Val Ala Arg Pro Thr Glu Val Leu Ala
242      115     120     125
243 Gly Thr Gln Leu Leu Tyr Ala Phe Phe Thr Arg Thr His Gly Asp Met
244      130     135     140
245 His Ser Leu Val Arg Ser Arg His Arg Ile Pro Glu Pro Glu Ala Ala
246 145     150     155     160
247 Val Leu Phe Arg Gln Met Ala Thr Ala Leu Ala His Cys His Gln His
248      165     170     175
249 Gly Leu Val Leu Arg Asp Leu Lys Leu Cys Arg Phe Val Phe Ala Asp
250      180     185     190
251 Arg Glu Arg Lys Lys Leu Val Leu Glu Asn Leu Glu Asp Ser Cys Val
252      195     200     205
253 Leu Thr Gly Pro Asp Asp Ser Leu Trp Asp Lys His Ala Cys Pro Ala
254      210     215     220
255 Tyr Val Gly Pro Glu Ile Leu Ser Ser Arg Ala Ser Tyr Ser Gly Lys
256 225     230     235     240
257 Ala Ala Asp Val Trp Ser Leu Gly Val Ala Leu Phe Thr Met Leu Ala
258      245     250     255
259 Gly His Tyr Pro Phe Gln Asp Ser Glu Pro Val Leu Leu Phe Gly Lys
260      260     265     270
261 Ile Arg Arg Gly Ala Tyr Ala Leu Pro Ala Gly Leu Ser Ala Pro Ala
262      275     280     285

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VERIFICATION SUMMARY

DATE: 03/25/2005

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Input Set : A:\3097USOP seq.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date